INHERITANCE OF ANTHRACNOSE RESISTANCE IN COMMON BEAN DIFFERENTIAL CULTIVARS TO, G 2333 AND AB 136

Ana Lilia Alzate-Marin¹, Henrique Menarim¹, Maricília C. C. de Arruda^{1,2}, Geraldo Assis de Carvalho¹, Trazilbo J. de Paula Jr.^{3,1}, Everaldo G. de Barros^{1,4} and Maurilio A. Moreira^{1,5}

¹BIOAGRO, ²ICNT/UNEMAT, ³EPAMIG, ⁴ Dept. de Biologia Geral; ⁵Dept. Bioquímica e Biologia Molecular – Universidade Federal de Viçosa, 36571-000 Viçosa, MG, Brasil.

Inheritance of anthracnose resistance of the common bean (*Phaseolus vulgaris*) differential cultivars TO, G 2333 and AB 136 to races 65, 73 and 89 of *Colletotrichum lindemuthianum* (binary system designation) was studied in crosses with the susceptible cultivar Rudá (Table 1). Rudá is a "carioca" type cultivar, with a good yield potential but susceptible to most races of the anthracnose fungus in Brazil. This cultivar is the recurrent progenitor in our backcross breeding program assisted by molecular markers for the creation of common bean cultivars resistant to anthracnose

For each experiment, the following number of seeds were sowed in the greenhouse in a completely randomized design: 30 seeds from each progenitor, 30 F_1 seeds; 171, 195, and 256 F_2 seeds (in crosses with TO, G 2333 and AB 136, respectively), and 60 seeds from each backcross (BCr and BCs). Fourteen days after sowing, the first expanded trifoliate leaf from each of the 405 plants was inoculated on the lower and upper surfaces with spore suspensions of *C. lindemuthianum* (1.2 x 10^6 spores/ml) with the aid of a horse-hair paint brush. The plants were then incubated for seven days in a mist chamber, which was maintained at $20 - 22^{\circ}$ C and 100% relative humidity. After this period, each plant was scored visually for the disease symptoms using a 1-9 scale based on Rava et al. (1993).

Our results (Tables 2-4) indicate that a single dominant gene controls resistance to races 65 and 89, giving a segregation ratio of 3:1 in the F_2 , 1:0 in the backcrosses to TO and AB 136 and 1:1 in the backcross to Rudá. For race 73, the following segregation ratios between resistant and susceptible plants were observed: 15:1 in the F_2 , 1:0 in the backcross to G 2333 and 3:1 in the backcross to Rudá. Such results suggest that two independent genes determine resistance of G 2333 to race 73.

This type of information is extremely important to our breeeding program as it will orient the search and identification of molecular markers linked to resistance genes to races 65, 89 and 73, which will facilitate the pyramiding of these genes in cultivar Rudá.

Table 1- Origin of isolates of Colletotrichum lindemuthianum^a used in the experiments

Race	Group/Race	Origin		
(system Binary)	(Classical Nomenclature)	(Brazilian State)		
65	ALFA/Epsilon	Espirito Santo		
73	ALFA/Alfa BR	Espirito Santo		
89	ALFA/Alfa BR	Minas Gerais		

*Rava et al., 1994.

Table 2- Segregation for resistance to Colletotrichum lindemuthianum race 65 in the cross Rudá x TO

		No. o	f Plants	Expected		
Pedigree	Generation	Resistant	Susceptible	ratio	χ²	Р
A285	P ₁	0	27	-	-	-
TO	P ₂	30	0	-	-	-
A 285 x TO	F ₁	17	0	-	-	-
A 285 x TO	F ₂	129	42	3:1	0.0060	0.95-0.98
F ₁ x A 285	BCs	29	30	1:1	0.0000	1.00
F ₁ x TO	BCr	56	0	1:0	0.0000	1.00

Table 3- Segregation for resistance to Colletotrichum lindemuthianum race 73 in the cross Rudá x G 2333

		No. o	f Plants	Expected		
Pedigree	Generation	Resistant	Susceptible	ratio	χ²	Р
A285	P ₁	0	22	-	-	•
G 2333	P ₂	24	0	-	-	-
A 285 x G 2333	F ₁	24	0	-	-	-
A 285 x G 2333	F ₂	181	14	15:1	0.150	0.50-0.70
F ₁ x A 285	BCs	27	19	3:1	5.680	0.01-0.02
F ₁ x G 2333	BCr	58	0	1:0	0.000	1.00

Table 4- Segregation for resistance to Colletotrichum lindemuthianum race 89 in the cross Rudá x AB 136

		No. of	Plants	Expected		
Pedigree	Generation	Resistant	Susceptible	ratio	χ²	Р
Rudá	P ₁	0	29	-	-	-
AB 136	P ₂	30	0	-	-	-
Rudá x AB 136	F ₁	29	0	-	-	-
Rudá x AB 136	F ₂	206	50	3:1	3.7968	0.10-0.05
F ₁ x Rudá	BCs	17	43	1:1	10.4167	0.01-0.00
F ₁ x AB 136	BCr	60	0	1:0	0.0000	1.00

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